GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003 16:51:22 ; Search time 81.8571 Seconds
(without alignments)
137.557 Million cell updates/sec

Title: US-09-856-070-16
Perfect score: 25
Sequence: 1 EREKE 5

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185234 seqs, [illegible] residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09856070_@CGN_1_1_448_@runat_14012003_155833_1511 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	21	21	AAZ77167	Human biallelic ma
	2	25	100.0	22	18	AAT90346	Heterogeneous nucl
	3	25	100.0	22	19	AAV07133	Nucleotide sequenc
c	4	25	100.0	22	20	AAX89363	Chromosomal bindin
c	5	25	100.0	25	22	AAC89617	S. cerevisiae YKR0
	6	25	100.0	27	22	AAD21712	Imperfect direct r
c	7	25	100.0	37	21	AAA56790	Multiple triplex r
c	8	25	100.0	37	21	AAA56792	Multiple triplex r
c	9	25	100.0	41	22	AAH79199	Human receptor-rel
c	10	25	100.0	47	24	ABK40858	Human obesity-asso
	11	25	100.0	49	13	AAQ33591	Microsatellite seq
	12	25	100.0	51	21	AAA76638	Human clone cg2530
	13	25	100.0	51	21	AAA76639	Human clone cg2530
	14	25	100.0	58	13	AAQ33612	Microsatellite seq
	15	25	100.0	60	24	ABN44740	Human spliced tran
c	16	25	100.0	63	20	AAH86904	Human single nucle
c	17	25	100.0	67	20	AAH86903	Human single nucle
	18	25	100.0	68	22	AAH37032	Human colon cancer
c	19	25	100.0	83	22	AAS23537	C. albicans essent
	20	25	100.0	92	22	ABA50927	Human breast cell
	21	25	100.0	92	22	ABA68905	Human foetal liver
	22	25	100.0	92	22	ABA35857	Probe #14323 for g
	23	25	100.0	92	22	AAK17237	Human brain expres
	24	25	100.0	92	22	AAK43024	Human bone marrow
	25	25	100.0	92	22	AAI23790	Probe #13723 for q
	26	25	100.0	92	22	AAI49100	Probe #17786 used
	27	25	100.0	92	22	AAI09397	Probe #9388 used t
	28	25	100.0	92	24	ABS17091	Human genome-deriv
	29	25	100.0	97	21	AAC12104	Human secreted pro
	30	25	100.0	103	22	AAL19504	Human breast cance
	31	25	100.0	106	21	AAC20101	Human secreted pro
c	32	25	100.0	107	21	AAA57245	Human breast cance
	33	25	100.0	108	24	ABK88533	Human cholecystoki
c	34	25	100.0	113	22	ABA71165	Human foetal liver
c	35	25	100.0	113	22	AAK19461	Human brain expres
c	36	25	100.0	113	22	AAK45451	Human bone marrow
c	37	25	100.0	113	22	AAI51396	Probe #20082 used
c	38	25	100.0	113	24	ABS19716	Human genome deriv
	39	25	100.0	115	22	ABA68275	Human foetal liver
	40	25	100.0	115	22	AAK16650	Human brain expres
	41	25	100.0	115	22	AAK42414	Human bone marrow
	42	25	100.0	115	22	AAI23172	Probe #13105 for q
	43	25	100.0	115	22	AAI48491	Probe #17177 used
	44	25	100.0	115	24	ABS16467	Human genome-deriv
	45	25	100.0	125	25	AAV87742	EST clone E097. H

ALIGNMENTS

RESULT 1
AAZ77167
ID AAZ77167 standard; DNA; 21 BP.
XX
AC AAZ77167;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:11523.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX

PN WO9954500 A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
XX
PS Claim 9; Page 2687; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID Nos 2852, 2912, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 21 BP; 13 A; 0 C; 7 G; 1 T; 0 other;

Alignment Scores:

Pred. No.:	75.7	Length:	21
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-856-070-16 (1-5) x AAZ77167 (1-21)

```
Qy       1 GluArgGluLysGlu 5
           |||||||||||||||
Db       2 GAGAGAGAAAAAGAG 16
```

RESULT 2
AAT90446
ID AAT90446 standard; DNA; 22 BP.
XX
AC AAT90446;
XX
DT 16-JAN-1998 (first entry)
XX
DE Heterogeneous nuclear ribonucleoprotein (hnRNP) gene probe.
XX
KW Epithelial protein; heterogeneous nuclear ribonuclear protein;
KW 703D4 antigen; hnRNP-A2; hnRNP-B1; lung cancer; liver cancer;
KW renal cancer; prostate cancer; melanoma; head cancer;
KW neck cancer; myeloma; marker; carcinogenesis; diagnosis; human;
KW probe; ss.
XX
OS Synthetic.
XX
PN WO9712975-A1.
XX
PD 10-APR-1997.
XX
PF 02-OCT-1996; 96WO-US15825.
XX
PF 02-OCT-1996; 96US-0725027.
PR 02-OCT-1995; 95US-0538711.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Mulshine JL, Tockman MS;
XX
DR WPI; 1997-226219/20.
XX
PT A new purified protein from epithelial cells is expressed in high
PT amounts in cancer and precancer cells; used as a marker for
PT diagnosis and treatment of cancer
XX
PS Example 1; Page 34; 171pp; English.
XX
CC This antisense oligonucleotide can be used as a probe in Southern
CC blot analysis of heterogeneous nuclear ribonucleoprotein (hnRNP)
CC sequences. An epithelial protein (see AAW26546-51) that shows
CC sequence homology to hnRNP A2/B1 is an early detection marker for
CC cancer, especially lung cancer.
XX
SQ Sequence 22 BP; 10 A; 3 C; 7 G; 2 T; 0 other;

Alignment Scores:

Pred. No.:	79.5	Length:	22
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-09-856-070-16 (1-5) x AAT90446 (1-22)

```
Qy       1 GluArgGluLysGlu 5
           |||||| ||||||||
Db       1 GAGAGAGAAAAGGAA 15
```

RESULT 3
AAV07133
ID AAV07133 standard; cDNA; 22 BP.
XX
AC AAV07133;
XX
DT 09-SEP-1998 (first entry)
XX
DE Nucleotide sequence of an antisense oligonucleotide.
XX
KW Ribonucleotide protein; hnRNPA2; human epithelial peptide; marker;
KW cancer; probe; hybridisation; primer; amplification; lung; liver;
KW kidney; breast; prostate; melanoma; myeloma; antibody; PCR; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9814469-A2.
XX
PD 09-APR-1998.
XX
PF 02-OCT-1997; 97WO-US17714.
XX
PR 02-OCT-1996; 96US-0725027.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Mulshine JL, Tockman MS;
XX
DR WPI; 1998-240016/21.

XX
PT New isolated epithelial protein as early marker of cancer - useful
PT in computer-assisted methods of diagnosis based on discriminant
PT analysis of optical images of cells
XX
PS Disclosure; Page 35; 159; English.
XX
CC This is the nucleotide sequence of an antisense oligonucleotide used
CC in the method of the invention. Probes and primers that hybridise to
CC or amplify these peptides are used to diagnose precancerous states,
CC e.g. of lung, liver, kidney, breast, prostate, head or neck, melanoma
CC or myeloma, or to determine susceptibility to these conditions and for
CC monitoring treatment. Precancer is also indicated by detecting
CC post-translational modification of the epithelial peptide which is a
CC marker of epithelial cell transformation. Antibodies are potentially
CC useful for diagnosisand treatment of cancer.
XX
SQ Sequence 22 BP; 10 A; 3 C; 7 G; 2 T; 0 other;

Alignment Scores:

Pred. No.:	79.5	Length:	22
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	19	Gaps:	0

US-09-856-070-16 (1-5) x AAV87133 (1-22)

```
Qy       1 GluArgGluLysGlu 5
           |||||||||||||||
Db       1 GAGAGAGAAAAGGAA 15
```

RESULT 4
AAX89363/c
ID AAX89363 standard; DNA; 22 BP.
XX
AC AAX89363;
XX
DT 24-SEP-1999 (first entry)
XX
DE Chromosomal binding site for p53 protein (Seq ID No: 9 of US5936079).
XX
KW Cell growth inhibition, chromosomal binding site, p53 protein;
KW cellular replication; cancer; ss.
XX
OS Synthetic.
XX
PN US5936079-A.
XX
PD 10-AUG-1999.
XX
PF 15-AUG-1994; 94US-0291011.
XX
PR 01-MAY-1992; 92US-0879618.
PR 06-APR-1992; 92US-0863661.
PR 15-AUG-1994; 94US-0291011.
XX
PA (ALTO-) ALTON OCHSNER MEDICAL FOUND.
XX
PI Cook J, Re R;
XX
DR WPI; 1999-457628/38.
XX
PT New oligonucleotide useful for treating and preventing cancer
XX
PS Claim 1; Column 12; 12pp; English.
XX
CC The invention provides methods for inhibiting cell growth by providing a
CC growing cell with an oligonucleotide capable of binding to a chromosomal
CC binding site for p53 protein. Sequences AAX89362, AAX89363 and AAX89366
CC represent oligonucleotides that are derived from the sequence AAX89355.
CC The oligonucleotides are used for inhibiting mammalian cellular
CC replication and the treatment and prevention of cancer in a human. The
CC oligonucleotides can be used in vitro to inhibit the growth of cultured
CC mammalian cells e.g. human, monkey, mouse, rat and hamster cells which
CC have chromosomal DNA encoding a binding site for p53 protein. Sequences
CC AAX89356-366 represent oligonucleotides that are based on chromosomal
CC binding sites for p53 protein.
XX
SQ Sequence 22 BP; 0 A; 7 C; 0 G; 15 T; 0 other;

Alignment Scores:

Pred. No.:	79.5	Length:	22
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-856-070-16 (1-5) x AAX89363 (1-22)

```
Qy       1 GluArgGluLysGlu 5
           |||||||||||||||
Db      22 GAAAGAGAAAAAGAA 8
```

RESULT 5
AAC89617/c
ID AAC89617 standard; DNA; 25 BP.
XX
AC AAC89617;
XX
DT 08-MAR-2001 (first entry)
XX
DE S. cerevisiae YKR079C gene PCR primer A.
XX
KW Yeast, germination, proliferation, essential gene, antifungal agent;
KW insecticide; herbicide; anti-proliferation drug; cancer; psoriasis;
KW restenosis, YKR083C; YFR003C, YGR277C, YGR278W; YKR071C; YKR079C;
KW YKR083C; PCR primer; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200071161-A1.
XX
PD 30-NOV-2000
XX
PF 12-MAY-2000; 2000WO-US13017.
XX
PR 21-MAY-1999; 99US-0315794.
PR 02-SEP-1999; 99US-0389341.
XX
PA (ROSE-) ROSETTA INPHARMATICS INC.
XX
PI Roberts CJ;
XX
DR WPI; 2001-025092/03.
XX
PT Identifying antifungal compounds which target yeast essential genes
PT comprises use of novel Saccharomyces cerevisiae essential genes
PT YFR003C, YGR277C, YGR278W, YKR071C, YKR079C or YKR083C or YKR081C -
XX
PS Example 5; Fig 28; 127pp; English.
XX
CC The present invention provides methods of identifying antifungal agents
CC using the coding and protein sequences of several yeast genes. These are
CC essential for the germination and proliferation of Saccharomyces
CC cerevisiae, and include YKR081C, YFR003C, YGR277C, YGR278W, YKR071C,
CC YKR079C and YKR083C. The sequences can also be used to identify compounds
CC for use as herbicides, insecticides and anti proliferation drugs which
CC can be used in the treatment of cancer, psoriasis and restenosis. This is
CC because they can be used to identify plant, insect and human homologues
CC of the yeast genes.
XX
SQ Sequence 25 BP; 4 A; 8 C; 1 G; 12 T; 0 other;

```
Alignment Scores:
Pred. No.:                90.9          Length:          25
Score:                    25.00         Matches:         5
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       22            Gaps:            0

US-09-856-070-16 (1-5) x AAC89617 (1-25)

Qy       1 GluArgGluLysGlu 5
           |||||||||||||||||
Db      19 GAGAGAGAAAAGGAG 5

RESULT 6
AAD21712
ID   AAD21712 standard; DNA; 27 BP.
XX
AC   AAD21712;
XX
DT   28-JAN-2002  (first entry)
XX
DE   Imperfect direct repeat #27 of human RPGR exon ORF15 repetitive sequence.
XX
KW   Human; mutation; retinitis pigmentosa GTPase regulator; RPGR;
KW   genotyping; open reading frame, ORF, X linked retinitis pigmentosa;
KW   XLRP; gene therapy; screening; forensic analysis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200177380 A2.
XX
PD   18-OCT-2001.
XX
PF   10-APR-2001; 2001WO-GB01622.
XX
PR   10-APR-2000; 2000GB-0008801
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Wright A;
XX
DR   WPI; 2001-663057/76.
XX
PT   Diagnosing disease or predisposition to disease, associated with
PT   disease causing mutations in retinitis pigmentosa GTPase regulator gene
PT   by genotyping ORF15 of the gene, and determining presence of mutations
PT   -
XX
PS   Disclosure; Fig 4E; 100pp; English.
XX
CC   The present invention relates to a method for diagnosing disease or
CC   predisposition to a disease, associated with a disease causing
CC   mutations in a retinitis pigmentosa GTPase regulator (RPGR) gene
CC   involves genotyping a RPGR gene, and determining whether the genotype
CC   comprises a disease causing mutations, where the risk genotype is
CC   present within open reading frame (ORF)15 of the RPGR gene. The method
CC   is useful for detecting a certain disease state e.g., X-linked
CC   retinitis pigmentosa (XLRP). The kit is useful for detecting and
CC   measuring disease causing mutations in biological fluids and tissues
CC   and for localising mutation in tissues. The mutant RPGR gene is useful
CC   in gene therapy techniques and for screening agents capable of
CC   affecting the expression of the sequences and/or the biological
CC   activity of mutant RPGR. They are preferably useful for identifying
CC   agonists and antagonists of RPGR. The mutant RPGR gene is also useful
CC   in identification of potential pharmaceutical targets in high
CC   throughput screening assays and forensic analysis. The present sequence
CC   is the imperfect direct repeat of human RPGR exon ORF15 repetitive DNA.
XX
SQ   Sequence 27 BP; 13 A; 0 C; 14 G; 0 U; 0 other;

Alignment Scores:
Pred. No.:                98.5          Length:          27
Score:                    25.00         Matches:         5
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       22            Gaps:            0

US-09-856-070-16 (1-5) x AAD21712 (1-27)

Qy       1 GluArgGluLysGlu 5
           |||||||||||||||||
Db       1 GAAAGGGAAAAGGAG 15

RESULT 7
AAA56790/c
ID   AAA56790 standard; DNA; 37 BP.
XX
AC   AAA56790;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Multiple triplex reporter forming probe MTRF7.
XX
KW   Multiple triplex reporter forming; MTRF; self-complexing;
KW   nucleic acid detection; signal amplification system;
KW   genetic hereditary testing; infectious disease; cancer;
KW   initiator probe; ss.
XX
OS   Synthetic.
XX
PN   WO200029624-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27525.
XX
PR   19-NOV-1998;   98US-0109082.
PR   27-JAN-1999;   99US-0117389.
PR   07-MAY-1999;   99US-0132976.
XX
PA   (CYGE-) CYGENE INC.
XX
PI   Ramberg ER;
XX
DR   WPI; 2000-387827/33.
XX
PT   Multiple Triplex Receptor Forming (MTRF) self-complexing probe
PT   composition useful for detection and analysis of nucleic acids,
PT   comprises an initiator probe and at least two MTRF probes -
XX
PS   Disclosure; Page 75; 142pp; English.
XX
CC   The present sequence is the multiple triplex receptor forming
CC   (MTRF) probe MTRF7. It is a component of a MTRF self-complexing probe
CC   composition which may be used for detection and analysis of nucleic
CC   acid sequences and for signal amplification. The composition comprises
CC   at least 2 MTRF probes and an initiator probe. The MTRF probes
CC   complex to the initiator probe to form triplex nucleic acid
CC   structures, which together form the self-complexing probe. The MTRF
CC   system may be used for direct RNA analysis and DNA diagnostic
CC   analysis. It is useful for early and sensitive detection of
CC   infectious disease and cancer and for genetic hereditary testing.
CC   The system provides high sensitivity and specificity and is easy to
CC   automate.
XX
SQ   Sequence 37 BP; 0 A; 15 C; 0 G; 20 T; 1 other;

Alignment Scores:
Pred. No.:                137           Length:          37
Score:                    25.00         Matches:         5
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       21            Gaps:            0
```

```
US-09-856-070-16 (1-5) x AAA56790 (1-37)

Qy      1 GluArgGluLysGlu 5
          ||||||||||||||||
Db     37 GAAAGAGAGAAGGAG 23

RESULT 8
AAA56792/c
ID   AAA56792 standard; DNA; 37 BP.
XX
AC   AAA56792;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Multiple triplex reporter forming probe MTRF9.
XX
KW   Multiple triplex reporter forming; MTRF; self-complexing;
KW   nucleic acid detection; signal amplification system;
KW   genetic hereditary testing, infectious disease; cancer;
KW   initiator probe; ss.
XX
OS   Synthetic.
XX
PN   WO200029624-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27525.
XX
PR   19-NOV-1998;   98US-0109082.
PR   27-JAN-1999;   99US-0117389.
PR   07-MAY-1999;   99US-0132976.
XX
PA   (CYGE-) CYGENE INC.
XX
PI   Ramberg ER;
XX
DR   WPI; 2000-387827/33.
XX
PT   Multiple Triplex Receptor Forming (MTRF) self-complexing probe
PT   composition useful for detection and analysis of nucleic acids,
PT   comprises an initiator probe and at least two MTRF probes -
XX
PS   Disclosure; Page 76, 142pp, English.
XX
CC   The present sequence is the multiple triplex receptor forming
CC   (MTRF) probe MTRF9. It is a component of a MTRF self-complexing probe
CC   composition which may be used for detection and analysis of nucleic
CC   acid sequences and for signal ampification. The composition comprises
CC   at least 2 MTRF probes and an initiator probe. The MTRF probes
CC   complex to the initiator probe to form triplex nucleic acid
CC   structures, which together form the self-complexing probe. The MTRF
CC   system may be used for direct RNA analysis and DNA diagnostic
CC   analysis. It is useful for early and sensitive detection of
CC   infectious disease and cancer and for genetic hereditary testing.
CC   The system provides high sensitivity and specificity and is easy to
CC   automate.
XX
SQ   Sequence 37 BP; 0 A; 16 C; 0 G; 20 T; 1 other;

Alignment Scores:
Pred. No.:              137          Length:        37
Score:                  25.00        Matches:       5
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     21           Gaps:          0

US-09-856-070-16 (1-5) x AAA56792 (1-37)

Qy      1 GluArgGluLysGlu 5
          ||||||||||||||||
Db     37 GAAAGAGAGAAGGAG 23

RESULT 9
AAH79199/c
ID   AAH79199 standard; DNA; 41 BP.
XX
AC   AAH79199;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human receptor-related protein tyrosine phosphatase 11 probe 1.
XX
KW   Human, receptor-related protein tyrosine phosphatase 11; cytostatic;
KW   virucidal; immunodulatory; antiinflammatory; haemostatic;
KW   malignant neoplasm; HIV; human immunodeficiency virus; infection;
KW   immunological disease; developmental disorder; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200166591-A1.
XX
PD   13-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-CN00213.
XX
PR   07-MAR-2000; 2000CN-0111925.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2001-589931/66.
XX
PT   Human receptor-related protein tyrosine phosphatase 11 and encoded
PT   polynucleotide for diagnosis and treatment of malignant neoplasm,
PT   haemopathy, HIV infection, immunological diseases and various
PT   inflammations -
XX
PS   Example 6; Page 15, 36pp; Chinese.
XX
CC   The invention relates to human receptor-related protein tyrosine
CC   phosphatase 11 and the encoding polynucleotide with cytostatic,
CC   virucidal, immunodulatory, antiinflammatory and haemostatic activity.
CC   The polypeptide and encoded polynucleotide are applicable in diagnosis
CC   and treatment of malignant neoplasm, haemopathy, HIV infection,
CC   immunological diseases, various inflammations and developmental
CC   disorders. The present sequence is that of a human receptor-related
CC   protein tyrosine phosphatase 11 probe, useful to the invention.
XX
SQ   Sequence 41 BP, 0 A, 16 C, 5 G, 20 T, 0 other;

Alignment Scores:
Pred. No.:              153          Length:        41
Score:                  25.00        Matches:       5
Percent Similarity:     100.00%      Conservative:  0
Best Local Similarity:  100.00%      Mismatches:    0
Query Match:            100.00%      Indels:        0
DB:                     22           Gaps:          0

US-09-856-070-16 (1-5) x AAH79199 (1-41)

Qy      1 GluArgGluLysGlu 5
          ||||||||||||||||
Db     34 GAAAGAGAGAAGGAA 20

RESULT 10
ABK40858/c
ID   ABK40858 standard; DNA; 47 BP.
XX
AC   ABK40858;
XX
DT   21-MAY-2002  (first entry)
XX
```

DE Human obesity-associated chromosome 3 biallelic marker #26.
XX
KW Human; obesity associated biallelic marker, chromosome 3, obesity; ds;
KW drug response; hyperuricaemia, digestive pathology, hypertension; cancer,
KW hepatic function disorder, cardiovascular disease, hyperlipidaemia;
KW insulin disorder; atheromatous disease; cardiac insufficiency.
XX
OS Homo sapiens.
XX
PN WO200206525-A2.
XX
PD 24-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-IB01477.
XX
PR 18-JUL-2000; 2000US-219704P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;
XX
DR WPI; 2002-155043/20.
XX
PT Set of novel map-related biallelic markers, preferably located on
PT obesity disorder-associated chromosomal regions on chromosomes 3, 10
PT and 19, useful, for e.g. detecting statistical correlations between
PT marker allele and a phenotype
XX
PS Claim 1; Page 214; 311pp; English.
XX
CC The invention relates to a set of novel map-related biallelic markers,
CC preferably located on obesity disorder-associated chromosomal regions on
CC chromosomes 3, 10 and 19. The markers are useful for genotyping or
CC estimating the frequency of an allele in a population, for detecting an
CC association between a genotype or haplotype and a phenotype, e.g. a
CC disease involving drug responses, obesity or disorders related to
CC obesity, such as hyperuricaemia, digestive pathology, hepatic function
CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,
CC insulin disorders, atheromatous disease and cardiac insufficiency. The
CC markers are useful for detecting a statistical correlation between a
CC biallelic marker allele and a phenotype and/or between a biallelic marker
CC haplotype and a phenotype. This sequence represents a human
CC obesity-associated biallelic marker located on chromosome 3
XX
SQ Sequence 47 BP, 8 A, 13 C, 2 G, 23 T, 1 other,

Alignment Scores:

Pred. No.:	176	Length:	47
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-070-16 (1-5) x ABK40858 (1-47)

```
Qy       1 GluArgGluLysGlu 5
           |||||||||||||||||
Db      18 GAAACAGACAAACAG 4
```

RESULT 11
AAQ33591
ID AAQ33591 standard; DNA; 49 BP.
XX
AC AAQ33591;
XX
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone AGLA285.
XX
KW PCR; selection, primers, OPTIPRIM, breeding, cattle, parentage,
KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7, Page 165, 517pp, English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (TG)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-34437.
XX
SQ Sequence 49 BP, 35 A, 0 C, 16 G, 0 U, 0 other;

Alignment Scores:

Pred. No.:	184	Length:	49
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-856-070-16 (1-5) x AAQ33591 (1-49)

```
Qy       1 GluArgGluLysGlu 5
           |||||||||||||||||
Db      24 GAGAGAGAGAAAGAG 38
```

RESULT 12
AAA76638
ID AAA76638 standard; cDNA; 51 BP.
XX
AC AAA76638;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone cg25309388 polymorphic site, SEQ ID NO:321.
XX
KW Human; single nucleotide polymorphism; SNP;
KW detection; identification; gene therapy; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	replace (26,T)
FT		/*tag= a

XX

```
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;   99WO-US27293
XX
PR   17-NOV-1998;   98US-0109024
PR   16-NOV-1999;   99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PI   for treating a subject suffering, or at risk from a pathology due to
PI   the presence of a sequence polymorphism -
XX
PS   Claim 1; Page 255; 543pp; English.
XX
CC   Sequences AAA76318 A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504-A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 51 BP; 20 A, 7 C, 15 G, 9 T, 0 other,

Alignment Scores:
Pred. No.:                192             Length:         51
Score:                    25.00           Matches:        5
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       21              Gaps:           0

US-09-856-070-16 (1-5) x AAA76638 (1-51)

Qy       1 GluArgGluLysGlu 5
           |||||||||||||||
Db      32 GAACGTGAAAAGGAA 46

RESULT 13
AAA76639
ID   AAA76639 standard; cDNA; 51 BP.
XX
AC   AAA76639;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cq25309388 polymorphic site, SEQ ID NO:322.
XX
KW   Human; single nucleotide polymorphism; SNP;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   variation       replace (26,C)
FT                   /*tag= a
XX
PN   WO200029623 A2.
XX
PD   25 MAY-2000.
XX
PF   17-NOV-1999;   99WO-US27293.
XX
PR   17-NOV-1998;   98US-0109024.
PR   16-NOV-1999;   99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism -
XX
PS   Claim 1, Page 255, 543pp; English.
XX
CC   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318 A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430 A77445) lead to conservative amino acid
CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504 A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 51 BP; 20 A, 6 C; 15 G; 10 T; 0 other;

Alignment Scores:
Pred. No.:                192             Length:         51
Score:                    25.00           Matches:        5
Percent Similarity:       100.00%         Conservative:   0
Best Local Similarity:    100.00%         Mismatches:     0
Query Match:              100.00%         Indels:         0
DB:                       21              Gaps:           0

US-09-856-070-16 (1-5) x AAA76639 (1-51)

Qy       1 GluArgGluLysGlu 5
           |||||||||||||||
Db      32 GAACGTGAAAAGGAA 46

RESULT 14
AAQ33612
ID   AAQ33612 standard; DNA; 58 BP.
XX
AC   AAQ33612;
XX
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone AGLA300.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
```

KW genetic mapping; traits; amplification; ss.
XX
OS Bos taurus.
XX
PN WO9213102-A.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92WO-US00340.
XX
PR 15-JAN-1991; 91US-0642342.
XX
PA (GENM) GENMARK.
XX
PI Georges M, Massey IM;
XX
DR WPI; 1992-284684/34.
XX
PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
XX
PS Table 7; Page 174; 517pp; English.
XX
CC The sequence is that of a bovine microsatellite sequence obtd by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC traits esp. in cattle, to allow selective breeding.
CC See also AAQ33501-33437
XX
SQ Sequence 58 BP; 30 A; 0 C; 28 G; 0 T; 0 other;

Alignment Scores:

Pred. No.:	220	Length:	58
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-856-070-16 (1-5) x AAQ33612 (1-58)

```
Qy       1 GluArgGluLysGlu 5
           ||||||||||||||||
Db       6 GAGAGAGAGAAAGAG 20
```

RESULT 15
ABN44740
ID ABN44740 standard; DNA; 60 BP.
XX
AC ABN44740;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:17488.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental specific genes -
XX
PS Example 1; SEQ ID 17488; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition, to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 36 A; 1 C; 22 G; 1 T; 0 other;

Alignment Scores:

Pred. No.:	228	Length:	60
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-070-16 (1-5) x ABN44740 (1-60)

```
Qy       1 GluArgGluLysGlu 5
           ||||||||||||||||
Db      14 GAGAGAGAGAAAGAA 28
```

Search completed: January 16, 2003, 17:19:25
Job time : 82.9821 secs